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## APPENDIX I

# Seq. Preps 2 hybrid-clones

Tubes

①	Pp1-8 ~	1.28 ug/tul	1.88
②	Pp55b-9 ~	reprep	
③	Tp16-5 ~	2.34 ug/tul	1.91
④	Tp22-4 ~	<del>2.67 ug/tul</del>	2.67 ug/tul 1.89
⑤	Pp1-1 ~	1.17 ug/tul	1.88
⑥	Tp86-10 ~	.78 ug/tul	1.96
⑦	Tp1-5 -	1.05 ug/tul	1.96
⑧	Pp63-9 -	.543 ug/tul	1.95
⑨	Pp55b-7 -	.611 ug/tul	1.93
⑩	Tp86-1 -	1.34 ug/tul	1.81

Tubes

Sequenced on

primers

①	Tp17-4.76	al used
②	Tp22E	1.87
→ ③	Pp1-1E	4.27
Nuis ④	Pp88E	2.17
↓ ⑤	Pp93E10	call wait
↓ ⑥	Tp8-1E	2.22

PAO<sup>11</sup>W



## APPENDIX II

PLAN

PB1

1001

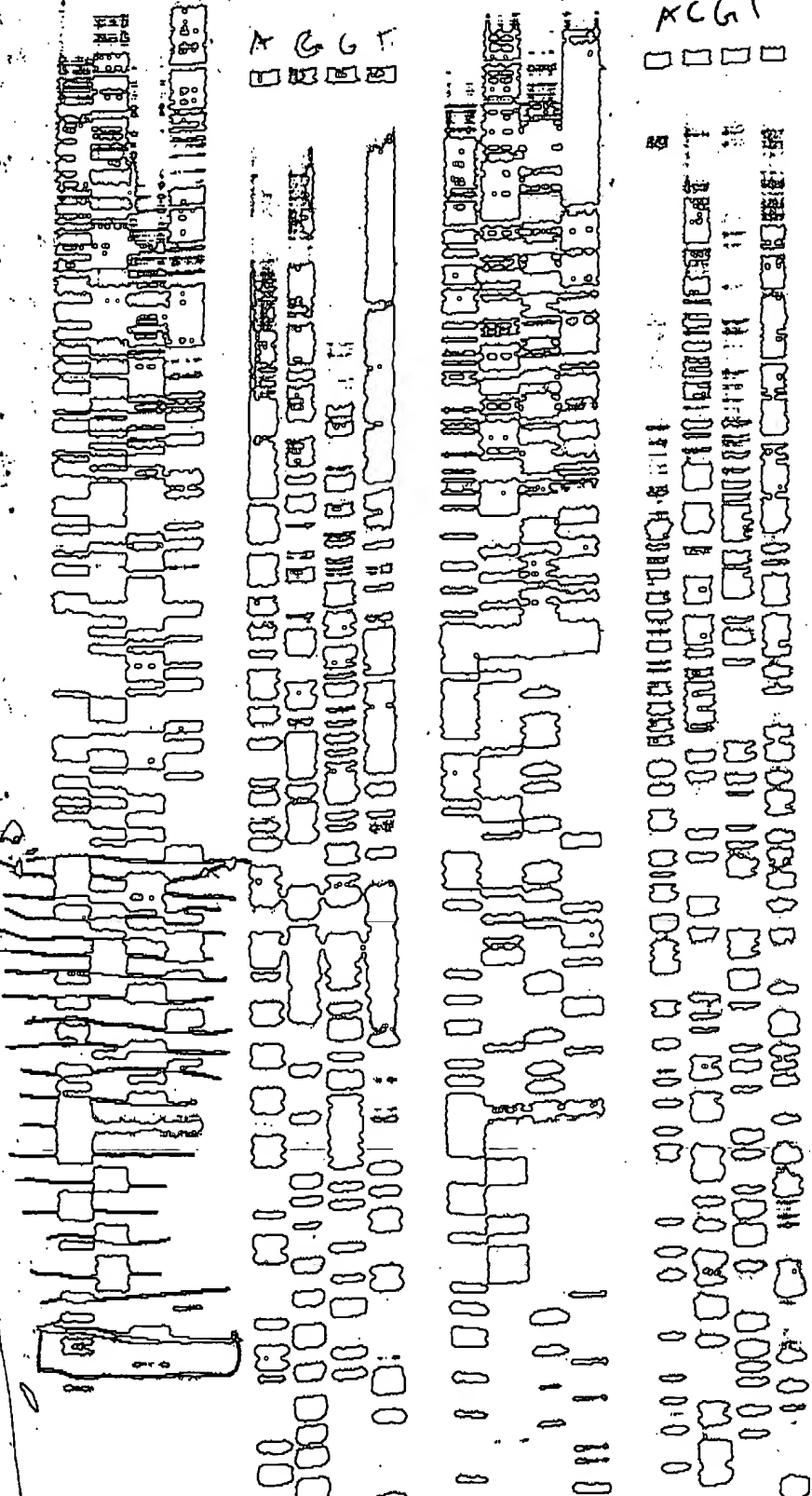
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1003  
1005



1911年 1月 1日

A detailed black and white line drawing of a complex, multi-story building. The structure features numerous windows of varying sizes, some with shutters or decorative elements. A central tower-like section rises above the main roofline. The drawing is oriented vertically, with the top of the building at the top of the page. The style is reminiscent of a technical or architectural sketch, with clean lines and no shading.

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## APPENDIX III

# BLAST Search Results

waiting for 7 jobs to finish

Commencing search, please wait for results.

BLASTN 2.0.5 [May-5-1998]

## Reference:

Altschul, Stephen F., Thomas L. Madden, Alejandro A. Schäffer, Jinghui Zhang, Zheng Zhang, Webb Miller, and David J. Lipman (1997), "Gapped BLAST and PSI-BLAST: a new generation of protein database search programs", Nucleic Acids Res. 25:3389-3402.

## Query=

(142 letters)

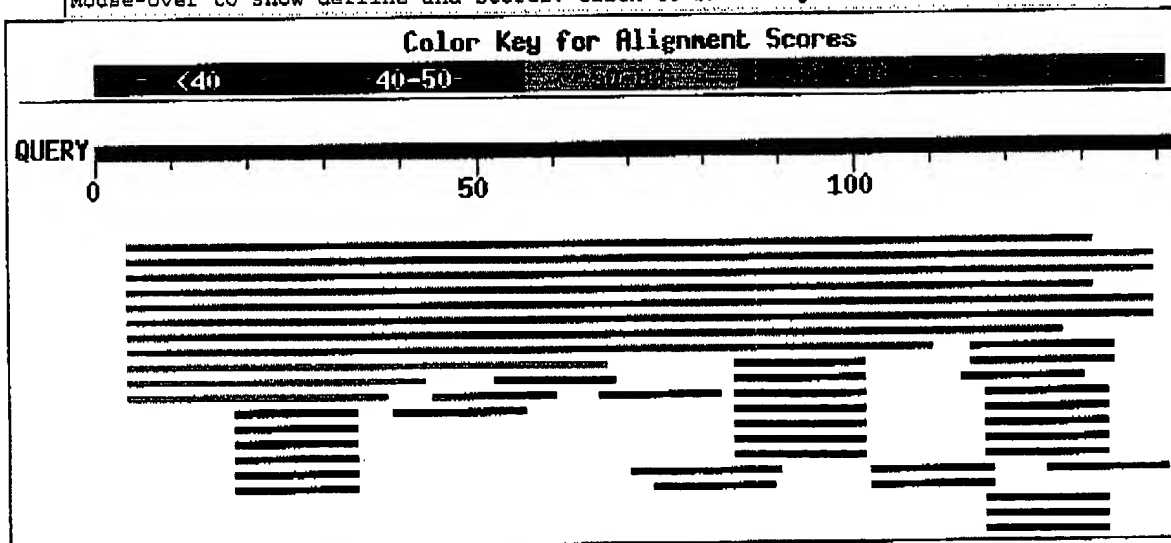
Database: Non-redundant Database of GenBank EST Division  
1,779,094 sequences; 669,153,423 total letters

Searching.....done

If you have any problems or questions with the results of this search  
please refer to the [BLAST FAQ](#)

## Distribution of 44 Blast Hits on the Query Sequence

Mouse-over to show defline and scores. Click to show alignments



Sequences producing significant alignments:

		Score (bits)	E Value	Kb
gb AA927260 AA927260	om17f11.s1 Soares_NFL_T_GBC_S1 Homo sapien...	198	1e-49	1.475
gb AA928789 AA928789	on98f03.s1 Soares_NFL_T_GBC_S1 Homo sapien...	196	5e-49	0.9
gb N21081 N21081	yx48f11.s1 Homo sapiens cDNA clone 265005 3'.	186	5e-46	1.391
gb AA719024 AA719024	ah46b10.s1 Soares testis NRT Homo sapiens ...	184	2e-45	?
gb AA909971 AA909971	ol11b04.s1 Soares_NFL_T_GBC_S1 Homo sapien...	182	7e-45	0.76
gb H16325 H16325	ym23a08.r1 Homo sapiens cDNA clone 48752 5'.	163	7e-39	1.355
gb N33318 N33318	yy08a03.s1 Homo sapiens cDNA clone 270604 3'.	147	4e-34	?
gb AA890309 AA890309	aj94f11.s1 Soares_parathyroid_tumor_NbMHPA ...	143	6e-33	?
gb AA514692 AA514692	nf58g03.s1 NCI_CGAP_Co3 Homo sapiens cDNA ...	66	1e-09	
gb AA099506 AA099506	zm17b06.r1 Stratagene pancreas (#937208) H...	66	1e-09	
emb Z44502 HSC22R121	H. sapiens partial cDNA sequence; clone c-...	50	7e-05	



gb AA010523 AA010523	zi09h05.r1 Soares fetal liver spleen INFLS...	40	0.065
gb AA447492 AA447492	zw90g11.r1 Soares total fetus Nb2HP8 9w Ho...	40	0.065
gb W97076 W97076	mf61a07.r1 Soares mouse embryo NbME13.5 14.5 M...	36	1.0
gb AA832749 AA832749	vw45h12.r1 Soares mouse mammary gland NbMM...	36	1.0
gb AA837370 AA837370	od41c01.s1 NCI_CGAP_GCB1 Homo sapiens cDNA...	36	1.0
gb AA555936 AA555936	vi64e02.r1 Beddington mouse embryonic regi...	36	1.0
gb AA866929 AA866929	vn42b08.r1 Stratagene mouse skin (#937313)...	36	1.0
gb W82751 W82751	mf06h09.r1 Soares mouse p3NMF19.5 Mus musculus...	36	1.0
gb H33571 H33571	EST109706 Rat PC-12 cells, NGF-treated (9 days...	36	1.0
gb AA050379 AA050379	mj14h07.r1 Soares mouse embryo NbME13.5 14...	36	1.0
gb W79090 W79090	EST01238 Homo sapiens cDNA clone HHCPR49.	34	4.0
gb AA121457 AA121457	zk91b06.r1 Soares pregnant uterus NbHPU Ho...	34	4.0
gb AA925855 AA925855	UI-R-A1-eo-e-08-0-UI.s1 UI-R-A1 Rattus nor...	34	4.0
gb W85717 W85717	zh55e01.s1 Soares fetal liver spleen INFLS S1 ...	34	4.0
gb AA206651 AA206651	zq56f07.r1 Stratagene neuroepithelium (#93...	34	4.0
gb AA224045 AA224045	zr11b09.r1 Stratagene hNT neuron (#937233)...	34	4.0
gb AA542501 AA542501	fa07c05.r1 Zebrafish ICRFzfls Danio rerio ...	34	4.0
gb AA295723 AA295723	EST100934 Pancreas tumor I Homo sapiens cD...	34	4.0
gb AA482424 AA482424	zt34f06.r1 Soares ovary tumor NbHOT Homo s...	34	4.0
gb AA055455 AA055455	zf20h09.r1 Soares fetal heart NbHH19W Homo...	34	4.0
gb R72686 R72686	yj93e02.r1 Homo sapiens cDNA clone 156314 5'.	34	4.0
gb AA074683 AA074683	zm76d06.r1 Stratagene neuroepithelium (#93...	34	4.0
gb AA205865 AA205865	zq50e06.r1 Stratagene neuroepithelium (#93...	34	4.0
gb T31062 T31062	EST26875 Homo sapiens cDNA 5' end similar to s...	34	4.0
gb T35967 T35967	EST94640 Homo sapiens cDNA 5' end similar to s...	34	4.0
gb AA639049 AA639049	ns02d08.s1 NCI_CGAP_Ew1 Homo sapiens cDNA ...	34	4.0
gb C28415 C28415	Rice cDNA, partial sequence (C61011_1A)	34	4.0
gb AA800626 AA800626	EST190123 Normalized rat lung, Bento Soare...	34	4.0
gb H75861 H75861	yu60g10.r1 Homo sapiens cDNA clone 230562 5'.	34	4.0
gb N86196 N86196	J7098F Fetal heart, Lambda ZAP Express Homo sa...	34	4.0
gb AA400442 AA400442	zu64a10.s1 Soares testis NHT Homo sapiens ...	34	4.0
gb AA100862 AA100862	zm26e04.r1 Stratagene pancreas (#937208) H...	34	4.0
gb AA293832 AA293832	zt65b11.r1 Soares testis NHT Homo sapiens ...	34	4.0

gb|AA927260|AA927260 om17f11.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 IMAGE:1541325 3'  
 Length = 350

1.175

Score = 198 bits (100), Expect = 1e-49  
 Identities = 128/132 (96%), Positives = 128/132 (96%), Gaps = 4/132 (3%)

Query: 5 gcaatcgagagcgttccccagttgg-tggccgtccggggc-ggaggggaagggagcctg 62  
 |||||  
 Sbjet: 214 gcaatcgagagcgttccccagttgggtggccgtccggggccggaggggaagggagcctg 273

Query: 63 gaatcc-aaccacctcccttgacagaccagcctgtc-agaatctagctgcctgagagag 120  
 |||||  
 Sbjet: 274 gaatcccaaccacctcccttgacagaccagcctgtccagaatctagctgcctgagagag 333

Query: 121 ggcgagaagggc 132  
 |||||  
 Sbjet: 334 ggcgagaagggc 345

gb|AA928789|AA928789 on98f03.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
 IMAGE:1564733 3'  
 Length = 480

Score = 196 bits (99), Expect = 5e-49  
 Identities = 136/142 (95%), Positives = 136/142 (95%), Gaps = 6/142 (4%)

Query: 5 gcaatcgagagcgttccccagttgg-tggccgtccggggc--ggaggggaagggagcct 61  
 |||||  
 Sbjet: 242 gcaatcgagagcgttccccagttgggtggccgtccggggccggaggggaagggagcct 301

Query: 62 ggaatcc-aaccacctcccttgacagaccagcctgtc-agaatctagctgcctgagaga 119  
 |||||  
 Sbjet: 302 ggaatcccaaccacctcccttgacagaccagcctgtccagaatctagctgcctgagaga 361

Query: 120 gggcgagaaggg-cagaatggg 140  
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Sbjct: 362 gggcgagaagggccagaatggg 383

gb|N21081|N21081 yx48f11.s1 Homo sapiens cDNA clone 265005 3'.  
Length = 461

Score = 186 bits (94), Expect = 5e-46  
Identities = 136/142 (95%), Positives = 136/142 (95%), Gaps = 6/142 (4%)

Query: 5 gcaatcgagagcggttccccagttgg-tggccgtccggggc-gga-ggggaagggagcct 61  
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Sbjct: 212 gcaatcgagagcggttccccagttgggtggccgtccggggcggagcgggaagggagcct 271

Query: 62 ggaatcc-aaccacctcccttgcagaccaggcctgtc-agaatctagctgcctgagaga 119  
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Sbjct: 272 ggaatcccaaccacctcccttgcagaccaggcctgtccagaatctagctgcctgagaga 331

Query: 120 gggcgagaaggg-cagaatggg 140  
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Sbjct: 332 gggcgagaagggccagaatggg 353

gb|AA719024|AA719024 ah46b10.s1 Soares testis NHT Homo sapiens cDNA clone 1292539 3'.  
Length = 433

Score = 184 bits (93), Expect = 2e-45  
Identities = 128/133 (96%), Positives = 128/133 (96%), Gaps = 5/133 (3%)

Query: 5 gcaatcgagagcggttccccagttgg-tggccgtccggggc-cggag-ggggaagggagcct 61  
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Sbjct: 217 gcaatcgagagcggttccccagttgggtggccgtccggggcaggagtggaagggagcct 276

Query: 62 ggaatcc-aaccacctcccttgcagaccaggcctgtc-agaatctagctgcctgagaga 119  
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Sbjct: 277 ggaatcccaaccacctcccttgcagaccaggcctgtccagaatctagctgcctgagaga 336

Query: 120 gggcgagaagggc 132  
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Sbjct: 337 gggcgagaagggc 349

gb|AA909971|AA909971 o111b04.s1 Soares\_NFL\_T\_GBC\_S1 Homo sapiens cDNA clone  
IMAGE:1523119 3'  
Length = 394

Score = 182 bits (92), Expect = 7e-45  
Identities = 136/143 (95%), Positives = 136/143 (95%), Gaps = 7/143 (4%)

Query: 5 gcaatcgagagcggttccccagttgg-tggccgtccggggc-ggagggg--aagggagcc 60  
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Sbjct: 242 gcaatcgagagcggttccccagttgggtggccgtccggggcggaggggggaagggagcc 301

Query: 61 tggaaatcc-aaccacctcccttgcagaccaggcctgtc-agaatctagctgcctgagag 118  
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Sbjct: 302 tggaaatcccaaccacctcccttgcagaccaggcctgtccagaatctagctgcctgagag 361

Query: 119 agggcgagaaggg-cagaatggg 140  
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Sbjct: 362 agggcgagaagggccagaatggg 384

gb|H16325|H16325 ym23a08.r1 Homo sapiens cDNA clone 48752 5'.  
Length = 435

Score = 163 bits (82), Expect = 7e-39  
Identities = 135/144 (93%), Positives = 135/144 (93%), Gaps = 8/144 (5%)

Query: 5 gcaatcgagagcggttccccagttgg-tggccgtccggggc-gga--ggggaaggagcc 60  
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Sbjct: 151 gcaatcgagagcggttccccagttgggtggccgtccggggccggatgggngaaggagcc 210

Query: 61 tgg-aatcc-aaccacctcccttgcagacccaggcctgtc-agaatctagctgcctgaga 117  
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Sbjct: 211 tgggaatcccaaccacctcccttgcagacccaggcctgtccagaatctagctgcctgaga 270

Query: 118 gagggcgagaaggc-cagaatggg 140  
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Sbjct: 271 gagggcgagaaggcccagaatggg 294

gb|N33318|N33318 yy08a03.s1 Homo sapiens cDNA clone 270604 3'.  
Length = 348

Score = 147 bits (74), Expect = 4e-34  
Identities = 122/131 (93%), Positives = 122/131 (93%), Gaps = 7/131 (5%)

Query: 5 gcaatcgagagcggttccccagttgg-tggccgtccggggc-ggagggg--aaggagcc 60  
|||||  
Sbjct: 211 gcaatcgagagcggttccccagttgggtggccgtccggggccgganggggaaggagcc 270

Query: 61 tggaatcc-aaccacctcccttgcagacccaggcctgt-cagaatct-agctgcctgaga 117  
|||||  
Sbjct: 271 tggaatcccaaccacctcccttgcagacccaggcctgtccagaatctaagctnccctgaga 330

Query: 118 gagggcgagaa 128  
|||||  
Sbjct: 331 gagggcgagaa 341

gb|AA890309|AA890309 aj94f11.s1 Soares\_parathyroid\_tumor\_NbHPA Homo sapiens cDNA clone  
IMAGE:1404141 3'  
Length = 329

Score = 143 bits (72), Expect = 6e-33  
Identities = 107/112 (95%), Positives = 107/112 (95%), Gaps = 5/112 (4%)

Query: 5 gcaatcgagagcggttccccagttgg-tggccgtccggggc-gga-ggggaaggagcct 61  
|||||  
Sbjct: 218 gcaatcgagagcggttccccagttgggtggccgtccggggccggatggggaaggagcct 277

Query: 62 ggaatcc-aaccacctcccttgcagacccaggcctgt-cagaatctagctgc 111  
|||||  
Sbjct: 278 ggaatcccaaccacctcccttgcagacccaggcctgtccagaatctagctgc 329

gb|AA514692|AA514692 nf58g03.s1 NCI\_CGAP\_Co3 Homo sapiens cDNA clone IMAGE:924148  
Length = 262

Score = 65.9 bits (33), Expect = 1e-09  
Identities = 40/41 (97%), Positives = 40/41 (97%), Gaps = 1/41 (2%)

Query: 5 gcaatcgagagcggttccccagtt-ggtggccgtccggggc 44  
|||||  
Sbjct: 218 gcaatcgagagcggttccccagttgggtggccgtccggggc 258

gb|AA099506|AA099506 zml7b06.r1 Stratagene pancreas (#937208) Homo sapiens cDNA clone  
525875 5'  
Length = 389

Score = 65.9 bits (33), Expect = 1e-09  
Identities = 63/70 (90%), Positives = 63/70 (90%), Gaps = 6/70 (8%)

Query: 5 gcaatcgagagcggttccccagttgg--tggcgcgtccgggg-cgga---ggggaaggag 58  
|||||  
Sbjct: 304 gcaatcgagagcggttccccagttgggtgggcgcgtccggggccgganggggggaaggag 363

Query: 59 cctggaatcc 68  
|||||  
Sbjct: 364 cctggaatcc 373

emb|Z44502|HSC22B121 H. sapiens partial cDNA sequence; clone c-22b12.  
Length = 191

Score = 50.1 bits (25), Expect = 7e-05  
Identities = 34/36 (94%), Positives = 34/36 (94%), Gaps = 1/36 (2%)

Query: 5 gcaatcgagagcggttccccagtt-ggtggccgtcc 39  
|||||  
Sbjct: 156 gcaatcgagagcgttccccagttgggtgggcgtcc 191

gb|AA010523|AA010523 zi09h05.r1 Soares fetal liver spleen INFLS S1 Homo sapiens cDNA  
clone 430329 5'  
Length = 303

Score = 40.1 bits (20), Expect = 0.065  
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 116 gagagggcgagaagggcaga 135  
|||||  
Sbjct: 4 gagagggcgagaagggcaga 23

gb|AA447492|AA447492 zw90g11.r1 Soares total fetus Nb2HF8 9w Homo sapiens cDNA clone  
784292 5' similar to WP:K07F5.14 CE06128 ;  
Length = 445

Score = 40.1 bits (20), Expect = 0.065  
Identities = 20/20 (100%), Positives = 20/20 (100%)

Query: 116 gagagggcgagaagggcaga 135  
|||||  
Sbjct: 27 gagagggcgagaagggcaga 46

gb|W97076|W97076 mf61a07.r1 Soares mouse embryo NbME13.5 14.5 Mus musculus cDNA  
clone 418740 5' similar to PIR:A49420 A49420 tuberous  
sclerosis protein 2 - human ;  
Length = 528

Score = 36.2 bits (18), Expect = 1.0  
Identities = 18/18 (100%), Positives = 18/18 (100%)

Query: 85 gaccagggcctgtcagaa 102  
|||||  
Sbjct: 160 gaccagggcctgtcagaa 143

gb|AA832749|AA832749 vw45h12.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone

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1246823 5' similar to TR:Q61008 Q61008 TUBERIN. ;  
Length = 561

Score = 36.2 bits (18), Expect = 1.0  
Identities = 18/18 (100%), Positives = 18/18 (100%)

Query: 85 gacccaggcctgtcagaa 102  
|||||  
Sbjct: 265 gacccaggcctgtcagaa 248

gb|AA837370|AA837370 od41c01.s1 NCI\_CGAP\_GCB1 Homo sapiens cDNA clone IMAGE:1370496  
similar to gb:D13748 EUKARYOTIC INITIATION FACTOR 4A-I  
(HUMAN);  
Length = 501

Score = 36.2 bits (18), Expect = 1.0  
Identities = 18/18 (100%), Positives = 18/18 (100%)

Query: 40 ggggcggaggggaagga 57  
|||||  
Sbjct: 468 ggggcggaggggaagga 451

gb|AA555936|AA555936 vi64e02.r1 Beddington mouse embryonic region Mus musculus cDNA  
clone 908570 5' similar to TR:G1236402 G1236402 TUBERIN.  
;  
Length = 390

Score = 36.2 bits (18), Expect = 1.0  
Identities = 18/18 (100%), Positives = 18/18 (100%)

Query: 85 gacccaggcctgtcagaa 102  
|||||  
Sbjct: 154 gacccaggcctgtcagaa 137

gb|AA866929|AA866929 vn42b08.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone  
1023831 5' similar to TR:Q61008 Q61008 TUBERIN. ;  
Length = 855

Score = 36.2 bits (18), Expect = 1.0  
Identities = 18/18 (100%), Positives = 18/18 (100%)

Query: 85 gacccaggcctgtcagaa 102  
|||||  
Sbjct: 591 gacccaggcctgtcagaa 608

gb|W82751|W82751 mf06h09.r1 Soares mouse p3NMF19.5 Mus musculus cDNA clone 404321 5'  
similar to PIR:A49420 A49420 tuberous sclerosis protein  
2 - human ;  
Length = 507

Score = 36.2 bits (18), Expect = 1.0  
Identities = 18/18 (100%), Positives = 18/18 (100%)

Query: 85 gacccaggcctgtcagaa 102  
|||||  
Sbjct: 321 gacccaggcctgtcagaa 304

gb|H33571|H33571 EST109706 Rat PC-12 cells, NGF-treated (9 days) Rattus sp. cDNA  
clone RPNAU10 5' end  
Length = 298

Score = 36.2 bits (18), Expect = 1.0  
Identities = 18/18 (100%), Positives = 18/18 (100%)